Sub Bundle

dehydrogenase], integrated into the chromosome, under conditions suitable for production of polyhydroxybutyrate-polyhydroxyvalerate by the transgenic organism.

1. (clean copy of amended claim) A method for the biological production of polyhydroxyalkanoate containing 3-hydroxyhexanoate comprising growing a transgenic organism selected from the group consisting of a transgenic bacterium and a transgenic plant having at least one bacterial transgene encoding an enzyme selected from the group consisting of a PHA polymerase incorporating C_6 substrates and a D-specific enoyl-CoA hydratase, integrated into the chromosome, under conditions suitable for production of polyhydroxybutyrate-polyhydroxyvalerate by the transgenic organism.

C1 cont'd.

2. (amended) The method of claim 1 wherein the organism is a [bacteria or] plant.

2. (clean copy of amended claim) The method of claim 1 wherein the organism is a plant.

3. (amended) The method of claim 2 wherein the organism is a plant selected from the group consisting of an oil crop [plants] plant and a starch accumulating [plants] plant.

3. (clean copy of amended) The method of claim 2 wherein the organism is a plant selected from the group consisting of an oil crop plant and a starch accumulating plant.

4. (amended) The method of claim 3 wherein the plant is selected from the group consisting of [Brassica] *Brassica*, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.

4. (clean copy of amended claim) The method of claim 3 wherein the plant is selected from the group consisting of *Brassica*, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.

5. (amended) The method of claim [2] 1 wherein the organism is a [bacteria] bacterium selected from the group consisting of *Escherichia, Klebsiella, Ralstonia, Alcaligenes, Pseudomonas,* and *Azotobacter*.

5. (clean copy of amended claim) The method of claim 1 wherein the organism is a bacterium selected from the group consisting of *Escherichia, Klebsiella, Ralstonia, Alcaligenes, Pseudomonas,* and *Azotobacter*.

7. (amended) The method of claim 6 wherein the [enzyme] polymerase is [derived] from *Aeromonas caviae, Comamonas testosteroni, Thiocapsia pfenigii, Chromatium vinosum, Bacillus cereus, Nocardia carolina, Nocardia salmonicolor, Rhodococcus ruber, Rhodcoccus rhodocrous,* and *Rhodospirilum rubrum*.

7. (clean copy of amended claim) The method of claim 6 wherein the polymerase is from *Aeromonas caviae, Comamonas testosteroni, Thiocapsia pfenigii, Chromatium vinosum, Bacillus cereus, Nocardia carolina, Nocardia salmonicolor, Rhodococcus ruber, Rhodcoccus rhodocrous,* and *Rhodospirilum rubrum*.

8. (amended) The method of claim 1 wherein the [organisms are] organism is genetically engineered to redirect metabolites to production of 3-hydroxyhexanoyl-CoA.

8. (clean copy of amended claim) The method of claim 1 wherein the organism is genetically engineered to redirect metabolites to production of 3-hydroxyhexanoyl-CoA.

9. (amended) The method of claim 8 wherein the [organisms are] organism is genetically engineered using a D-specific enoyl-CoA hydratase gene.

9. (clean copy of amended claim) The method of claim 8 wherein the organism is genetically engineered using a D-specific enoyl-CoA hydratase gene.

10. (amended) The method of 9 wherein the hydratase gene is isolated from a [bacteria] bacterium selected from the group consisting of *R. eutropha, Klebsiella aerogenes, P. putida,* and *Aeromonas caviae.*

10. (clean copy of amended claim) The method of 9 wherein ~~the~~ hydratase gene is isolated from a bacterium selected from ~~the~~ group consisting of *R. eutropha, Klebsiella aerogenes, P. putida, ~~and~~ Aeromonas caviae.*

11. (amended) The method of claim 8 wherein the [organisms are] organism is genetically engineered using the genes encoding the enzymes in a butyrate fermentation pathway.

11. (clean copy of amended claim) The method of claim 8 wherein the organism is genetically engineered using the genes encoding the enzymes in a butyrate fermentation pathway.

12. (amended) The method of claim 11 wherein the enzymes in the butyrate fermentation pathway [is] are from *Clostridium acetobutylicium* or *Thermoanaerobacterium thermosaccharolyticum.*

12. (clean copy of amended claim) The method of claim 11 wherein the enzymes in the butyrate fermentation pathway are from *Clostridium acetobutylicium* or *Thermoanaerobacterium thermosaccharolyticum.*

13. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to convert butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.

Sub D6 cont'd

[13. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to convert butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.]

14. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a broad range reductase that is active on C_6 substrates.

[14. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a broad range reductase that is active on C_6 substrates.]

15. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a polymerase that accepts 3-hydroxyhexanoyl CoA.

C2 cont'd

[15. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a polymerase that accepts 3-hydroxyhexanoyl CoA.]

16. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a thiolase accepting acetoacetyl CoA.

[16. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a thiolase accepting acetoacetyl CoA.]

17. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express an enzyme selected from the group consisting of thiolases specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, [PHA polymerase that accepts 3-hydroxybutyryl CoA] and 3-hydroxyhexanoyl CoA.

[17. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express an enzyme selected from the group consisting of thiolases

specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, and 3-hydroxyhexanoyl CoA.]

18. (amended) The method of claim 8 wherein the [organisms are] organism is further genetically engineered [using] to express one or more fatty acid biosynthetic enzymes.

18. (clean copy of amended claim) The method of claim 8 wherein the organism is further genetically engineered to express one or more fatty acid biosynthetic enzymes.

22. (amended) The method of claim 18 wherein the enzymes are [derived] from *E. coli*.

[22. (clean copy of amended claim) The method of claim 18 wherein the enzymes are from *E. coli*.]

23. (amended) The method of claim 8 wherein the [organisms are] organism is further genetically engineered [using a] to express one or more enzymes forming a fatty acid oxidation complex.

23. (clean copy of amended claim) The method of claim 8 wherein the organism is further genetically engineered to express one or more enzymes forming a fatty acid oxidation complex.

25. (amended) The method of claim 24 wherein the enzymes are [derived] from *Nocardia salmonicolor*.

[25. (clean copy of amended claim) The method of claim 24 wherein the enzymes are from *Nocardia salmonicolor*.]

26. (amended) The method of claim 24 wherein the epimerizing enzymes [for epimerization] are [derived] from the *Pseudomonas putida* FaoAB complex.